



EXHIBIT A

>Monday, March 21, 2005

>DNA59844 [Full]

>685 sites [All Sites]

[DNA59844], avagts (oligo)

[DNA59844], sheldens

> Lib309

tail

snabi

nlalii thal maeli/hpyCH4IV

sphi fnudII/mvni

nsphi bstUI

hpy99I hpyCH4V rsal

tail nspl bsh1236I

hnlII/acyI cac8I csp6I

sapi alui ahaliI/bsaHI mlui bsaAI

mboII aaliiI cac8I aflIII alui apoi

sfcI earI/kep632I maeli/hpyCH4IV bslwI/spII hpy188I

1 GACACTATATAG AAGAGCTATG ACGTCGCATG CACGCGTAC TAAGCTCGGA ATTGGCTCG AGCAGGATGC AGGCGCGGCT GCGAGGAGC TGCCTCTC

CTGTGATATC TTCTCGATAC TGCAGCGTAC GTGCGCATGC ATTGAGCCT TAAGCCGAGC TCGTCTTACG TCCCGGCGCA CCGTCCCTCG ACGGAGGAG

1

^insert starts here

^MET

59844.AV393.f, Stag=TTTTTGAATTCTAACCACAC^

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scrFI[dcm-]      haeIII/palI
pspGI            stuI[dcm-]
mvaI             scrFI[dcm-]
ecorII[dcm-]     pspGI
dsav[dcm-]       mvaI          bsaXI
bstNI            ecorII[dcm-]  mspI
bssKI[dcm-]      dsav[dcm-]    hpaII
bslI[dcm-]       mboII          scrFI[M.hpaII-]
cac8I apyI[dcm+] bssKI[dcm-]  nciI
haeIII/palI      apyI[dcm+]    dsav      mnli
sau96I[M.haeIII-] bbsI      bsaJI mnli  bssKI sfaNI bseRI
101 TGGGCCTGCT CCTGGTCTGT CTTCATCTCC CAGGCCTCTT TGCCCGGAGC ATCGGTGTTG TGGAGGAGAA AGTTTCCCAA AACTTCGGGA CCAACTTGCC
ACCCGGACGA GGACCAGACA GAAGTAGAGG GTCCGGAGAA ACGGCCTCG TAGCCACAAC ACCTCCTCTT TCAAGGGTT TTGAAGCCTT GGTGAACGG
13  G L L L V C L H L P G L F A R S I G V V E E K V S Q N F G T N L P
^59844.AV395.Ef, 5tag=TTTTTATGCATCAGATGACGATGACAAA

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[illegible]

GSeqEdit, DNA59844 [Full], page 3

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sau3AI
mboI/ndelI[dam-]
dpnII[dam-]
dpnI[dam+]
nlaIV
bstYI/xhoII
bamHI
alwI[dam-]
mnlI styI
ddeI alwI[dam-]
bspCNI bsajI
401 CTGAGGATCC TTGGCAGATG ATGGCTGCTG CGGCTGAGGA CGGCTGGGG GAAGCGCTGC CTGAAGAACT CTCTTACCTC TCCAGTCTG CGGCCCTCGC
GACTCCTAGG AACCGTCTAC TACCGACGAC GCCGACTCCT GCGGACCC CTTCCGCGAG GACTTCTTGA GAGAATGGAG AGGTCACGAC GCGGGGAGCG
113 E D P W Q M M A A A E D R L G E A L P E E L S Y L S S A A A L A

scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
tseI sau96I dsav[dcM-] tseI
fnu4HI/bsoFI bstNI fnu4HI/bsoFI
bbvI avall bssKI[dcM-] bbvI
tseI ddeI bsajI hinPI
mwoI fnu4HI/bsoFI apyI[dcM+] hhaI/cfoI mboII
fnu4HI/bsoFI mnlI bslI haeII eco57I
bbvI acII bspCNI acII afeI/eco47III
401 CTGAGGATCC TTGGCAGATG ATGGCTGCTG CGGCTGAGGA CGGCTGGGG GAAGCGCTGC CTGAAGAACT CTCTTACCTC TCCAGTCTG CGGCCCTCGC
GACTCCTAGG AACCGTCTAC TACCGACGAC GCCGACTCCT GCGGACCC CTTCCGCGAG GACTTCTTGA GAGAATGGAG AGGTCACGAC GCGGGGAGCG
113 E D P W Q M M A A A E D R L G E A L P E E L S Y L S S A A A L A

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scrFI[dcM-]      pleI
pspGI            mlyI
mvaI             hinfI
ecORI[dcM-]      scrFI[dcM-]
dsaV[dcM-]       pspGI
mboII            mvaI
ecORI[dcM-]       ecorII[dcM-]
dsaV[dcM-]        dsaV[dcM-] pleI
bstNI            bstNI hpy188I
bssKI[dcM-]      mnII  bssKI[dcM-] hpy188III
bsaJI pleI       econI
apyI[dcM+]       mlyI
sau96I[M.haeIII-] bbsI
haeIII/palI      haeIII/palI
bslI[dcM-] mlyI  bslI[dcM-] ahdI/eam1105I
tsprI            stuI hphI mnII bseRI apyI[dcM+] hinfI
bslI[dcM-] hinfI hpy188III
TCCGGGCAGT GGCCTTTGC CTGGGGAGTC TTCTCCCGAT GCCACAGGCC TCTCACCTGA GGCTTCACTC CTCCACCAGG ACTCGGAGTC CAGACGACTG
AGGCCCGTCA CCGGGAACG GACCCCTCAG AAGAGGGCTA CCGTGTCGG AGAGTGGACT CCGAAGTCAG GAGGTGGTCC TGAGCCTCAG GTCTGCTGAC
146 P G S G P L P G E S S P D A T G L S P E A S L L H Q D S E S R R L

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scrFI[dcM-]
pspGI
mvaI   rsaI
ecorII[dcM-]
dsaV[dcM-]
bstNI  csp6I
bssKI[dcM-]
bsaJI  nlaIV
bsaJI  kpnI
        hphI apyI[dcM+]
sau3AI[M.hphI-]
mboI/ndeII[dcM-]
dpnII[dcM-]  banI
dpnI[dcM+]  asp718
        bclI[dcM-]  acc65I
601 CCCCGTTCTA ATTCACTGGG AGCCGGGGGA AAAATCCTTT CCCAAGCCC TCCCTGGTCT CTCATCCACA GGGTTCTGCC TGATCACCCC TGGGGTACCC
GGGGCAAGAT TAACTGACCC TCGGCCCCCT TTTTAGGAAA GGGTTGGGG AGGACCCAGA GAGTAGGTGT CCCAAGACGG ACTAGTGGGG ACCCATGGG
179 P R S N S L G A G G K I L S Q R P P W S L I H R V L P D H P W G T L

        bsmAI
        bsaI
scrFI[dcM-]
pspGI
mvaI
        ecorII[dcM-]
dsaV[dcM-]
bstNI
bssKI[dcM-]
bsaJI  foki
        mnlI apyI[dcM+]  bstF5I
scrFI[M.hpaiI-]
ncII
mspI
hpaiI
dsaV
bsrI  bssKI
tspRI  bsaJI
        tsp509I  nlaIV

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rsal
csp6I
nlaIV
kpnI
bani
asp718[dcM-]
acc65I[dcM-]
xcmI
scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
dsaV[dcM-]
bstNI
bssKI[dcM-]
apyI[dcM+]
bsaJI
801 CCCAGGTACC AGCTGGGGA ATATTATCG GTATCCAGGA GGCAGCTGGG GAAATATTAA TCGGTATCCA GGAGGCAGCT GGGGGATAT TAATCGGTAT
GGGTCCATGG TCGACCCCTT TATAATTAGC CATAGTCCCT CCGTCGACCC CTTATAATT AGCCATAGGT CCTCCGTCGA CCCCCTTATA ATTAGCATA
246 P G T S W G N I N R Y P G G S W G N I N R Y

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sau96I[dcM-][M.haeIII-]

haeIII/palI

eco0109I/draII[dcM-]

alwNI[dcM-]

alw26I/bsmAI

scrFI[dcM-] pciI

pspGI nspHI

mvaI hpaI nlaIII

ecoRII[dcM-] nspI

dsaV[dcM-] tru9I

bsp1286 bstNI hincII/hindII

bmyI bssKI[dcM-] aflIII

banII apyI[dcM+] mseI

mwoI

tspRI mnlI

1101 TGTGTGGGCT CAATCCAGGC CCTGTTAACA TGTTCAGC ACTATCCCA CTTTCAGTG CCTCCCTGC TCATCTCAA TAAATATAA GCATTATGA
ACACACCCGA GTTAGTCCG GGACAATTGT ACAAAGTGTG TGATAGGGT GAAAGTCAC GGAGGGGACG AGTAGAGGT ATTTTATTTT CGTGAATACT

mc
ea
ea
cf
bs
not
fnu
aci

1201 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

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scrFI[M.hpaII-]
ncii
mspI
hpaII
dsaV          rsal
xmaI/pspAI    sau96I
smaI          mroI   nlaIV
scrFI[M.hpaII-] rsrII/cspI
ncii          hpy188III csp6I
dsaV          bspMII kpnI
alul salI bsaKI      bspEI banI sfcI
sstI hincII/hindII[M.taqI-] avall[M.hpaII-]
sacI accI[M.taqI-] tru9I cpoI asp718 cac8I
rmaI hgiAI/aspHI[M.aluI-] mseI bsaWI cfr10I/bsrFI
maeI ecl136II bsaJI aseI/asnI/vspI acc65I hpyCH4V
bfai bsp1286[M.aluI-] xmnI tsp509I bsaWI pstI
acII speI bsiHKAi taqI bsaKI tsp509I mspI ageI sse8387I
fnu4HI/bsoFI bmyI hpy99I avai[M.hpaII-] hpaII mspI bspMI rsal
haeIII/palI banII[M.aluI-] asp700 accIII hpaII sbfI csp6I aluI sfcI hinfI aluI
1301 GCGCGGCGAC TAGTGAGCTC GTCGACCGCG GAATTAATTC CGGACCGGTA CCTGCAGGCG TACCAGCTTT CCTATAGTG AGTCGTATTA GAGCTTGG
CCGGCGGCTG ATCACTCGAG CAGCTGGGCC CTTAATTAAG GCCTGGCCAT GGAGTCCGC ATGCTCGAAA GGGATATCAC TCAGCATAAT CTCGAACC

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> length: 1398

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aatII(GACGTC):      20
acc65I(GGTACC):    694 805 1347
accI(GTAKAC):      1321
accIII(TCCGGA):    1339

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75 247 254 430 441 490 969 1090 1299 1303

20

453

32 1128

1344

20

262 580

14 43 88 203 299 811 844 877 910 999 1316 1365 1392

1116

405 406

1116

49

111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976

1115

823 856 889 1333

823 856 889 1333

1331

694 805 1347

1044 1315

57 1326

188 261 438 1342

265 1024

932

405

694 805 1347

1106 1315

119 528

89 249 375 424 427 456 487 842 875 908

59 752

831 864 897

aciI (CCGC) :

acyI (GRCGYC) :

afeI (AGCGCT) :

aflIII (ACRYGT) :

ageI (ACCGGT) :

ahaII (GRCGYC) :

ahdI (GACNNNNNGTC) :

aluI (AGCT) :

alw26I (CAGNNNCTG) :

alwI (GGATCNNNN) :

alwNI (CAGNNNCTG) :

apoI (RAATTY) :

apyI (CCWGG) :

aseI (ATTAAT) :

asnI (ATTAAT) :

asp700 (GAANNNTTC) :

asp718 (GTACC) :

aspHI (GWGCWC) :

avaI (CYCGRG) :

avaII (GGWCC) :

avrII (CCTAGG) :

baeI (NNNNNNNNNNNNACNNNGTAYCNNNNNNNNNN) :

bamHI (GGATCC) :

banI (GGYRCC) :

banII (GRCGYC) :

bbsI (GAAGACNNNNN) :

bbvI (GCACC) :

bcgI (NNNNNNNNNNCGANNNNNTGCNNNNNNNNNN) :

bciVI (GTATCC) :

bclI (TGATCA) :	681
bfaI (CTAG) :	266 1025 1041 1310
bglI (GCNNNNNGGC) :	971
blnI (CCTAGG) :	265 1024
blpI (GCTNAGC) :	300
bmyI (GDGCHC) :	1044 1106 1315
bpmI (CTGGAG) :	480 959
bpu1102I (GCTNAGC) :	300
bpuAI (GAAGACNNNNNN) :	119 528
bsaAI (YACGTR) :	37
bsaHI (GRCGYC) :	20
bsaI (GGTCTCNNNN) :	656
bsaJI (CCNNGG) :	129 265 383 409 444 520 623 652 688 689 716 732 733 801 933 1024
	1326
bsaWI (WCCGGW) :	1339 1344
bsaXI (NNNNNNNNNACNNNNCTCCNNNNNNNN) :	146 1072
bseRI (GAGGAGNNNNNNNN) :	95 163 568
bsgI (GTGCAG) :	349
bsh1236I (CGCG) :	33 76
bsiEI (CGRYCG) :	1300
bsiHKAI (GWGCWC) :	1044 1315
bsiWI (CGTACG) :	35
bslI (CCNNNNNNGG) :	105 199 313 328 331 364 441 495 502 514 570 576 733 1062 1063
bsmAI (GTCTC) :	657
bsmAI (GTCTC) :	657
bsmFI (GGGACNNNNNNNNNNNN) :	187 736
bsoFI (GCNGC) :	74 89 249 375 424 427 430 456 487 490 842 875 908 1299 1302
bsp1286 (GDGCHC) :	1044 1106 1315
bspCNI (CTCAGNNNNNNNNNN) :	200 301 401 434 557 770
bspEI (TCCGGA) :	1339

bspMI (ACCTGC) : 330 1350
 bspMII (TCCGGA) : 1339
 bsrBI (GAGCGG) : 254
 bsrFI (RCCGGY) : 1344
 bsrI (ACTGNN) : 223 482 615 707 739
 bssKI (CCNGG) : 111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901
 934 958 976 1115 1326 1327
 bstDSI (CCRYGG) : 383
 bstF5I (GGATG) : 65 244 663 993
 bstNI (CCWGG) : 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
 1115
 bstUI (CGCG) : 33 76
 bstYI (RGATCY) : 405
 bsu36I (CCTNAGG) : 400 556 769
 btgI (CCRYGG) : 383
 btsI (GCAGTGNN) : 346 506 1032
 cac8I (GCNNGC) : 26 30 104 252 305 378 1000 1354
 celII (GCTNAGC) : 300
 cfoI (GCGC) : 92 454
 cfr10I (RCCGGY) : 1344
 cfrI (YGGCCR) : 1300
 cpoI (CGGWCCG) : 1341
 csp6I (GTAC) : 36 695 806 1348 1360
 cspi (CGGWCCG) : 1341
 ddeI (CTNAG) : 200 301 401 434 557 770
 dpnI (GATC) : 406 682
 dpnII (GATC) : 406 682
 draII (RGGNCCY) : 729 1117
 dsal (CCRYGG) : 383
 dsav (CCNGG) : 111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901

eaeI (YGGCCR) :	934 958 976 1115 1326 1327
eagI (CGGCCG) :	1300
eam1105I (GACNNNNNGTC) :	1300
earI (CTCTTCNNNN) :	262 580
ecfI (GGCGGA) :	10 981
ecf136II (GAGCTC) :	968
ecfXI (CGGCCG) :	1315
eco47III (AGCGCT) :	1300
eco57I (CTGAAG) :	453
eco81I (CCTNAGG) :	295 461
ecoNI (CCTNNNNNAGG) :	400 556 769
ecoO109I (RGGNCCY) :	331 570
ecori (GAATTC) :	729 1117
ecorII (CCWGG) :	49
espI (GCTNAGC) :	111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
fnu4HI (GCNGC) :	1115
fnuDII (CGCG) :	300
fokI (GGATG) :	74 89 249 375 424 427 430 456 487 490 842 875 908 1299 1302
gsuI (CTGGAG) :	33 76
haeII (RGCICY) :	65 244 663 993
haeIII (GGCC) :	480 959
hglAI (GWCWC) :	453
hhaI (GCGC) :	73 103 133 226 359 395 492 511 547 730 755 1118 1301
hinPI (GCGC) :	1044 1315
hincII (GTYRAC) :	92 454
hindII (GTYRAC) :	92 454
hinfI (GATC) :	1124 1321
hinII (GRCGYC) :	1124 1321
	388 526 580 586 702 776 1079 1380
	20

hpaI (GTTAAC) : 1124
 hpaII (CCGG) : 144 502 623 1327 1340 1345
 hphI (GGTGA) : 553 684
 hpy188I (TCNGA) : 46 206 238 294 316 583
 hpy188III (TCNNGA) : 185 258 534 589 1339
 hpy99I (CGWCG) : 22 1320
 hpyCH4IV (ACGT) : 21 38
 hpyCH4V (TGCA) : 29 68 333 345 350 1031 1353
 kpnI (GGTACC) : 694 805 1347
 ksp632I (CTCTTCNNNN) : 10 981
 maeI (CTAG) : 266 1025 1041 1310
 maeII (ACGT) : 21 38
 mboI (GATC) : 406 682
 mboII (GAAGA) : 10 120 463 529 982
 mcrI (CGRYCG) : 1300
 mluI (ACGCGT) : 32
 mlyI (GAGTCNNNNN) : 526 580 586 1079 1380
 mnII (CCTC) : 97 135 163 199 218 230 292 310 338 354 361 403 436 477 495 549 559
 570 649 722 728 753 772 839 872 905 955 973 1015 1054 1161
 mroI (TCCGGA) : 1339
 mseI (TTAA) : 824 857 890 1125 1334
 mspAII (CMGCKG) : 810 843 876 909 998
 mspI (CCGG) : 144 502 623 1327 1340 1345
 mstII (CCTNAGG) : 400 556 769
 mvaI (CCWGG) : 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
 1115
 mvnI (CGCG) : 33 76
 mwoI (GCNNNNNNNGC) : 300 351 424 490 971 1099 1160
 nciI (CCSGG) : 143 502 623 1326 1327
 ncoI (CCATGG) : 383

ndeII (GATC) :	406 682
nlaIII (CATG) :	27 384 759 1129
nlaIV (GGNCC) :	187 226 261 288 395 405 619 694 805 1347
notI (GGGCGCG) :	1299
nspBII (CMGCKG) :	810 843 876 909 998
nspHI (RCATGY) :	26 1128
nspI (RCATGY) :	26 1128
paer7I (CTCGAG) :	57
pali (GGCC) :	73 103 133 226 359 395 492 511 547 730 755 1118 1301
pciI (ACATGT) :	1128
pflMI (CCANNNNTGG) :	313
pleI (GAGTCNNN) :	526 580 586 1079 1380
pspAI (CCCGGG) :	1326
pspGI (CCWGG) :	111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
	1115
pstI (CTGCAG) :	332 344 1352
pvuII (CAGCTG) :	810 843 876 909 998
rmaI (CTAG) :	266 1025 1041 1310
rsaI (GTAC) :	36 695 806 1348 1360
rsrII (CGGWCCG) :	1341
sacI (GAGCTC) :	1315
sali (GTCGAC) :	1321
sapI (GCTCTTCNNN) :	10 980
sau3AI (GATC) :	406 682
sau96I (GGNCC) :	72 102 188 226 261 395 438 492 511 730 755 1118 1342
sauI (CCTNAGG) :	400 556 769
sbfI (CCTGCAGG) :	331 1351
scrFI (CCNGG) :	111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901
	934 958 976 1115 1326 1327
sfaNI (GCATC) :	66 149 538

sfcI (CTRYAG) :	5 332 344 1352 1373
smaI (CCCGGG) :	1326
smlI (CTYRAG) :	57
snaBI (TACGTA) :	37
speI (ACTAGT) :	1309
sphI (GCATGC) :	26
splI (CGTACG) :	35
sse8387I (CCTGCAGG) :	331 1351
sspiI (AATATT) :	820 853 886 919
sstiI (GAGCTC) :	1315
stuiI (AGCCT) :	132 546
styI (CCWGG) :	265 383 409 1024
taiiI (ACGT) :	21 38
taqiI (TCGA) :	58 1322
tfiiI (GAWTC) :	388 702 776
thaiI (CGCG) :	33 76
tliiI (CTCGAG) :	57
tru9I (TTAA) :	824 857 890 1125 1334
tseI (GCWGC) :	89 249 375 424 427 456 487 842 875 908
tsp509I (AATT) :	50 610 1332 1336
tspRI (NNCAGTGNN) :	222 347 483 507 614 708 1033 1156
vspI (ATTAAT) :	823 856 889 1333
xcmI (CCANNNNNNTTGG) :	802 835 868 901
xhoI (CTCGAG) :	57
xhoII (RGATCY) :	405
xmaI (CCCGGG) :	1326
xmaIII (CGCCCG) :	1300
xmnI (GAANNNNTTC) :	1331

not found:

acII (AACGTT), afII (CTTAAG), ahaIII (TTTAAA), alw44I (GTGCAC), apaI (GGGCCC), apaLI (GTGCAC), ascI (GGCGCGCC), aspi (GACNNNGTC),
 avaiII (ATGCAT), aviII (TGGCA), bali (TGGCA), bbrPI (CACGTG), bceAI (ACGGCNNNNNNNNNN), bfrBI (ATGCAT), bfrI (CTTAAG),
 bglII (AGATCT), bsaBI (GATNNNATC), bsiCI (TTCGAA), bsmBI (CGTCTCNNNN), bsmI (GAATGCN), bsp106 (ATCGAT), bsp120I (GGGCCC),
 bsp1407I (TGTACA), bspCI (CGATCG), bspDI (ATCGAT), bspHI (TCATGA), bsrDI (GCAATGNN), bsrGI (TGTACA), bssHII (GGCGGC),
 bssSI (CTCGTG), bst1107I (GTATAC), bst4CI (ACNGT), bstAPI (GACNNNNNGTC), bstBI (TTCGAA), bsteII (GCTNACC), bstXI (CCANNNNNNNTGG),
 bstZ17I (GTATAC), btrI (CACGTC), claI (ATCGAT), draI (TTTAAA), draII (CACNNNGTG), drdI (GACNNNNNGTC), eco72I (CACGTG),
 ecoRV (GATATC), eheI (GGCGCC), esp3I (CGTCTC), fseI (GGCGCGCC), fspI (TGCACA), hgaI (GACGC), hindIII (AAGCTT), hpyCH4III (ACNGT),
 kasI (GGCGCC), kspI (CCGCGG), maeII (GTNAC), mamI (GATNNNNATC), mfeI (CAATTG), mscI (TGGCCA), mslI (CAYNNNNRTG), muni (CAATTG),
 naeI (GGCGGC), narI (GGCGCC), ndeI (CATATG), ngoMI (GCCGGC), nheI (GCTAGC), nruI (TCGCA), nsiI (ATGCAT), paci (TTAATTAA),
 pflFI (GACNNNGTC), pmeI (GTTAAAC), pmlI (CACGTG), ppul10I (ATGCAT), ppulMI (RGWCCY), pshAI (GACNNNGTC), psiI (TTATAA),
 psp1406I (AACGTT), pspOMI (GGGCCC), pvuI (CGATCG), rcaI (TCATGA), sacII (CCGCGG), sandI (GGWCCC), scaI (AGTACT),
 sceI (TAGGGATAACAGGGTAAT), sexAI (ACWGGT), sfii (GGCCNNNNNGGCC), sfuI (TTCGAA), sgfi (GGCATCGC), sgrAI (CRCCGGYG),
 snoI (GTGCAC), snoI (GTGCAC), srfi (GCCCGGGC), sstII (CCGCGG), swaI (ATTTAAAT), tsp45I (GTSAC), tth111I (GACNNNGTC), xbaI (TCTAGA)